

SCORE Search Results Details for Application 10552515 and Search Result 20080624_083145_us-10-552-515-1.rag.

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This page gives you Search Results detail for the Application 10552515 and Search Result 20080624_083145_us-10-552-515-1.rag.

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GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: June 24, 2008, 08:32:16 ; Search time 263 Seconds
(without alignments)
2135.186 Million cell updates/sec

Title: US-10-552-515-1
Perfect score: 4950
Sequence: 1 MRMAATAWAGLQGPPLPTLC.....SELSSHWTPTFTVPKASQLQQ 933

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3405708 seqs, 601879884 residues

Total number of hits satisfying chosen parameters: 3405708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200711:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000:*
4: geneseqp2001:*
5: geneseqp2002:*
6: geneseqp2003a:*
7: geneseqp2003b:*
8: geneseqp2004a:*

9: geneseqp2004b:*
 10: geneseqp2005:*
 11: geneseqp2006:*
 12: geneseqp2007:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4950	100.0	933	8	ADT77664	Adt77664 Splice va
2	4950	100.0	933	11	AEL84788	Ael84788 Tumor mar
3	4531.5	91.5	885	10	AEB13426	Aeb13426 Human pro
4	4364.5	88.2	843	10	AEB13424	Aeb13424 Human pro
5	3736	75.5	898	4	ABG15488	Abg15488 Novel hum
6	1531.5	30.9	920	6	ADB64420	Adb64420 Human pro
7	1511.5	30.5	920	6	ABP58666	Abp58666 Human dih
8	1504	30.4	981	8	ADK52114	Adk52114 Human ato
9	1504	30.4	981	12	AEN06206	Aen06206 Human eso
10	1489	30.1	1017	12	AFB77190	Afb77190 Mouse TM-
11	1488	30.1	960	11	AEG11142	Aeg11142 Human tra
12	1479.5	29.9	840	11	AEG11146	Aeg11146 Human tra
13	1464	29.6	1003	7	ADG48280	Adg48280 Human ret
14	1455	29.4	913	11	AEH82071	Aeh82071 Human gna
15	1445	29.2	1219	4	ABB62812	Abb62812 Drosophil
16	1445	29.2	1219	10	AFB95185	Afb95185 Fruit fly
17	1402.5	28.3	910	6	ADC42854	Adc42854 REMAP pro
18	1402.5	28.3	910	11	AEL84658	Ael84658 Tumor mar
19	1369.5	27.7	1075	4	ABB65993	Abb65993 Drosophil
20	1369.5	27.7	1075	10	AFC04729	Afc04729 Fruit fly
21	1367.5	27.6	712	11	AEG11145	Aeg11145 Human tra
22	1199.5	24.2	1058	4	ABB65022	Abb65022 Drosophil
23	1199.5	24.2	1058	10	AFC01816	Afc01816 Fruit fly
24	1154	23.3	596	6	ADB64387	Adb64387 Human pro
25	1061.5	21.4	594	4	AAB92637	Aab92637 Human pro
26	1061.5	21.4	594	5	ABP43811	Abp43811 FLJ10261
27	1061.5	21.4	594	8	ADJ75429	Adj75429 Marker ge
28	1061.5	21.4	594	8	ADN04848	Adn04848 Antipsori
29	1061.5	21.4	594	11	AEG11143	Aeg11143 Human FLJ
30	1037.5	21.0	782	6	ADX42387	Adx42387 Human col
31	1037.5	21.0	782	7	ADT95905	Adt95905 Colon can
32	1037.5	21.0	782	8	ADQ96288	Adq96288 T cell ac
33	1037.5	21.0	782	8	ADQ96104	Adq96104 T cell ac
34	912.5	18.4	475	6	ADB64962	Adb64962 Human pro
35	905	18.3	642	7	ADM05798	Adm05798 Human pro

36	905	18.3	642	10	AEC88728	Aec88728 Human cDN
37	905	18.3	642	11	AEG11144	Aeg11144 Human FLJ
38	819.5	16.6	443	5	ABP41785	Abp41785 Human ova
39	817.5	16.5	179	6	AAO29613	Aao29613 Human Nov
40	784.5	15.8	390	5	ABB90382	Abb90382 Human pol
41	735	14.8	139	5	AAE24066	Aae24066 Human pro
42	722.5	14.6	360	4	AAM40391	Aam40391 Human pol
43	711.5	14.4	346	8	ADP29628	Adp29628 Human sec
44	695.5	14.1	608	8	ADQ96298	Adq96298 T cell ac
45	695.5	14.1	608	8	ADQ96286	Adq96286 T cell ac

ALIGNMENTS

RESULT 1

ADT77664

ID ADT77664 standard; protein; 933 AA.

XX

AC ADT77664;

XX

DT 15-JUN-2007 (revised)

DT 13-JAN-2005 (first entry)

XX

DE Splice variant-novel gene expressed in prostate (SV-NGEP) polypeptide.

XX

KW Splice variant-novel gene expressed in prostate; SV-NGEP; human;

KW prostate cancer; cytostatic; gene therapy; immunotherapy; BOND_PC;

KW NGEP long variant; NGEP long variant [Homo sapiens]; G05886.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 1. .345

FT /label= Cytoplasmic

FT Region 157. .933

FT /note= "An immunogenic fragment comprising 8 consecutive amino acids that specifically binds to an antibody that specifixally binds to a polypeptide comprising amino acids 157-933 is referred to in Claim 1"

FT Region 170. .178

FT /note= "Epitope, predicted to bind HLA2-01"

FT Region 215. .223

FT /note= "Epitope, predicted to bind HLA2-01"

FT Region 258. .266

FT /note= "Epitope, predicted to bind HLA2-01"

FT Domain 346. .368

FT /label= Transmembrane

FT Domain 369. .421

FT		/label= External
FT		/note= "Cell surface"
FT	Region	403. .411
FT		/note= "Epitope, predicted to bind HLA2-01"
FT	Domain	422. .441
FT		/label= Transmembrane
FT	Region	427. .435
FT		/note= "Epitope, predicted to bind HLA2-01"
FT	Domain	442. .501
FT		/label= Cytoplasmic
FT	Domain	502. .524
FT		/label= Transmembrane
FT	Domain	525. .543
FT		/label= External
FT		/note= "Cell surface"
FT	Domain	544. .566
FT		/label= Transmembrane
FT	Region	557. .565
FT		/note= "Epitope, predicted to bind HLA2-01"
FT	Region	562. .570
FT		/note= "Epitope, predicted to bind HLA2-01"
FT	Domain	567. .586
FT		/label= Cytoplasmic
FT	Domain	587. .609
FT		/label= Transmembrane
FT	Domain	610. .714
FT		/label= External
FT		/note= "Cell surface"
FT	Domain	715. .737
FT		/label= Transmembrane
FT	Domain	738. .761
FT		/label= Cytoplasmic
FT	Domain	762. .784
FT		/label= Transmembrane
FT	Domain	785. .933
FT		/label= External
FT		/note= "Cell surface"
FT	Region	846. .854
FT		/note= "Epitope, predicted to bind HLA2-01"
XX		
PN	WO2004092213-A1.	
XX		
PD	28-OCT-2004.	
XX		
PF	05-APR-2004; 2004WO-US010588.	
XX		
PR	08-APR-2003; 2003US-0461399P.	
XX		
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	

WPI; 2004-758338/74.
N-PSDB; ADT77665.
PC:NCBI; gi48093524.

Claim 1; SEQ ID NO 1; 88pp; English.

Revised record issued on 15-JUN-2007 : Enhanced with precomputed information from BOND.

Sequence 933 AA;

Query Match	100.0%;	Score 4950;	DB 8;	Length 933;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 933;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

Db	1	MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAERWAMTSETSSGSHCARSRMLRRA	60
Qy	61	QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQQAACRAGSPAKPRIADFLVWEEDL	120
Db	61	QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQQAACRAGSPAKPRIADFLVWEEDL	120
Qy	121	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLC	180
Db	121	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLC	180
Qy	181	YYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLEVVPDVPPEYYSCRFRVNKLPRF	240
Db	181	YYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLEVVPDVPPEYYSCRFRVNKLPRF	240
Qy	241	LGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT	300
Db	241	LGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT	300
Qy	301	PPEGPQAPRLNQRVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA	360
Db	301	PPEGPQAPRLNQRVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA	360
Qy	361	AVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDH	420
Db	361	AVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDH	420
Qy	421	GGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	480
Db	421	GGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	480
Qy	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSNTLLAAW	540
Db	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSNTLLAAW	540
Qy	541	ASRIASLTGSVNVLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNIFY	600
Db	541	ASRIASLTGSVNVLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNIFY	600
Qy	601	SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV	660
Db	601	SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV	660
Qy	661	LIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI	720
Db	661	LIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI	720
Qy	721	FVAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	780
Db	721	FVAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	780

Qy	781	AFLLAFFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTCERYAFRDDDGHYS	840
Db	781	AFLLAFFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTCERYAFRDDDGHYS	840
Qy	841	QTYWNLLAIRLAFVIVFEHVVSFVGRLDLLVPDIPESVEIKVKREYYLAKQALAENEVL	900
Db	841	QTYWNLLAIRLAFVIVFEHVVSFVGRLDLLVPDIPESVEIKVKREYYLAKQALAENEVL	900
Qy	901	FGTNGTKDEQPKGSELSSHWTPFTVTPKASQLQQ	933
Db	901	FGTNGTKDEQPKGSELSSHWTPFTVTPKASQLQQ	933

RESULT 2

AEL84788

ID AEL84788 standard; protein; 933 AA.

XX

AC AEL84788;

XX

DT 18-OCT-2007 (revised)

DT 15-JUN-2007 (revised)

DT 28-DEC-2006 (first entry)

XX

DE Tumor marker gene NGEP SEQ ID NO 155.

XX

KW cytostatic; diagnosis; prognosis; tumor marker; gene expression;

KW drug screening; cancer; neoplasm; NGEP; BOND_PC; NGEP long variant;

KW GO5886.

XX

OS Homo sapiens.

XX

PN WO2006110593-A2.

XX

PD 19-OCT-2006.

XX

PF 07-APR-2006; 2006WO-US013172.

XX

PR 07-APR-2005; 2005US-0669342P.

PR 11-OCT-2005; 2005US-0725982P.

XX

PA (MACR-) MACROGENICS INC.

XX

PI Von Haller PD, Schummer M, Meyer DW, Schubert LA, Tjoelker LW;

XX

DR WPI; 2006-814687/82.

DR N-PSDB; AEL84787.

DR REFSEQ; NP_001001891.

DR PC:NCBI; gi48093524.

XX

PT Detecting or diagnosing cancer in a subject comprises determining
PT expression of at least one gene, and comparing level of expression to a
PT control sample from a normal subject, where increased expression level
PT indicates cancer.

XX

PS Claim 8; SEQ ID NO 155; 583pp; English.

XX

CC The invention describes a method of detecting or diagnosing cancer in a
CC subject comprising determining the expression level of at least one gene,
CC and comparing the level of expression to a corresponding control sample
CC from a normal subject, where cancer is detected or diagnosed if there is
CC an increase in the expression level of the gene relative to the
CC expression in the control sample. Also described are: identifying a
CC compound to be tested for its ability to prevent, treat, manage, or
CC ameliorate cancer or its symptom; a compound identified by the method;
CC treating cancer in a patient; treating a cancer in a subject that is
CC fully or partially refractory to a first treatment in a patient; and a
CC pharmaceutical composition comprising an amount of an antibody selected
CC from anti-SLC12A2, anti-FLJ23375, anti-GRM5, anti-TAS2R1, anti-NRXN2,
CC anti-C14orf160, anti-MGC 15668, anti-MGC33486, anti-TMEM16F, anti-FAT,
CC anti-KIAA0195, anti-LRFN, anti-NFASC, anti-BAT2D1, anti-MGC2963, anti-
CC KIAA0685, anti-EDG3, anti-GGTL3, anti-PLVAP, anti-FLJ31528, anti-
CC FLJ90709, anti-VEZATIN, anti-TMPRSS9, anti-ATP13A5, anti-PKHD1L1, anti-
CC C2orf18, anti-ANKRD22, anti-FAM62B, anti-LOC57168, anti-CDKAL1, anti-
CC SLC39A3v1, anti-SLC39A3v2, anti-BAT5, anti-TM9SF4, anti-DC2, anti-VAPB,
CC anti-XTP3TPB, anti-TACSTD2, anti-FNDC3A, anti-GK001, anti-OCIAD2, anti-
CC PR01855, anti-C20orf3, anti-SDFR1, anti-FLJ20481, anti-LENG4, anti-
CC FLJ12443, anti-ARP5 Long, anti-ARP5 Short, anti-TMD0645, anti-NGEP, anti-
CC IL1RAP1, anti-PLXNB1, anti-ATP2B2, anti-FLJ11848, anti-ENTPD2, anti-
CC PPM1H, anti-KRTKAP3, anti-KCNC3, anti-TM9SF1, anti-ULBP1, anti-C19orf26,
CC anti-KIAA830, anti-KIAA1244, anti-KIAA1797, anti-MGC26856, anti-NETO2,
CC anti-SUSD2, anti-FOLR2, anti-EMR2, ENTPD1, anti-ATP10B, anti-PTK7, anti-
CC FLJ14681, anti-C20orf22, anti-FLJ14281, anti-FAM8A1, anti-TMED7, anti-
CC C20orf108, anti-ATAD1, anti-GPR154, anti-C14orf27, anti-OSAP, anti-
CC FAD104, anti-FLJ90492, anti-SLC27A3, anti-RON, anti-ATP13A1, anti-
CC DKFZP564D166, anti-ESSPL, anti-EXTL3, anti-KAI1, anti-KIAA0960, anti-
CC MTRNL, anti-SLC27A1, anti-GRIA, anti-OR4M1, anti-KIAA1679, or anti-UPK-1b
CC antibody, and a pharmaceutical carrier. The methods are useful for
CC detecting, diagnosing, and treating cancer, e.g. colon, lung, ovary,
CC prostate, pancreas, or bladder cancer. This is the amino acid sequence of
CC NGEP, altered levels of expression are useful in the diagnosis or
CC prognosis of cancer.

CC

CC Revised record issued on 18-OCT-2007 : Enhanced with precomputed
CC information from BOND.

XX

SQ Sequence 933 AA;

Query Match 100.0%; Score 4950; DB 11; Length 933;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 933; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAERWAMTSETSSGSHCARSRMLRRA	60
Db	1	MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAERWAMTSETSSGSHCARSRMLRRA	60
Qy	61	QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQQAACRAGSPAKPRIADFLVWEE	120
Db	61	QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQQAACRAGSPAKPRIADFLVWEE	120
Qy	121	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLC	180
Db	121	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLC	180
Qy	181	YYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLEVPDVPPEYYSCRFRVKNLPRF	240
Db	181	YYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLEVPDVPPEYYSCRFRVKNLPRF	240
Qy	241	LGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT	300
Db	241	LGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT	300
Qy	301	PPEGPQAPRLNQRVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA	360
Db	301	PPEGPQAPRLNQRVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA	360
Qy	361	AVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDH	420
Db	361	AVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDH	420
Qy	421	GGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	480
Db	421	GGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	480
Qy	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVSRSGNTLLAAW	540
Db	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVSRSGNTLLAAW	540
Qy	541	ASRIASLTGSVNVLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFI	600
Db	541	ASRIASLTGSVNVLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFI	600
Qy	601	SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV	660
Db	601	SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV	660
Qy	661	LIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCGLFDEYLEMVLQFGFVTI	720

Db	661	 LIPKLGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI	720
Qy	721	FVAACPLAPLFPALLNNWVEIRLDARKEVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	780
Db	721	 FVAACPLAPLFPALLNNWVEIRLDARKEVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	780
Qy	781	AFLLEAFSSDFLPRAYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTCERYAFRDDDGHYS	840
Db	781	 AFLLEAFSSDFLPRAYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTCERYAFRDDDGHYS	840
Qy	841	QTYWNLLAIRLAFVIVFEHVVFVSVGRLLDLLVPDIPESVEIKVKREYYLAKQALAENEVL	900
Db	841	 QTYWNLLAIRLAFVIVFEHVVFVSVGRLLDLLVPDIPESVEIKVKREYYLAKQALAENEVL	900
Qy	901	FGTNGTKDEQPKGSELSSHWTPFTVPKASQLQQ	933
Db	901	 FGTNGTKDEQPKGSELSSHWTPFTVPKASQLQQ	933

RESULT 3
AEB13426

ID	AEB13426	standard; protein; 885 AA.
XX		
AC	AEB13426;	
XX		
DT	22-SEP-2005	(first entry)
XX		
DE	Human prostate specific polypeptide #2.	
XX		
KW	Screening; diagnosis; drug delivery; prostate specific polypeptide;	
KW	cancer; prostate tumor; cytostatic; neoplasm.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2005062788-A2.	
XX		
PD	14-JUL-2005.	
XX		
PF	16-DEC-2004; 2004WO-US042406.	
XX		
PR	22-DEC-2003; 2003US-0531809P.	
XX		
PA	(AVAL-) AVALON PHARM INC.	
XX		
PI	Weigle B, Ebner R;	
XX		
DR	WPI; 2005-497793/50.	
DR	N-PSDB; AEB13425.	

Db	63	 QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQQAACRAGSPAKPRI-DFVLVWEEDL	121
Qy	121	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLC	180
Db	122	 KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLC	181
Qy	181	YYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLEVVPDVPPEYYSCRFRVKNKLPRF	240
Db	182	 YYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLEVVPDVPPEYYSCRFRVKNKLPRF	241
Qy	241	LGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT	300
Db	242	 LGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT	301
Qy	301	PPEGPQAPRLNQRVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA	360
Db	302	 PPEGPQAPRLNQRVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA	361
Qy	361	AVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDH	420
Db	362	 AVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDH	421
Qy	421	GGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	480
Db	422	 GGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	481
Qy	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVVSRSGNTLLAAW	540
Db	482	 TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVVSRSGNTLLAAW	541
Qy	541	ASRIASLTGSVNVLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFY	600
Db	542	 ASRIASLTGSVNVLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFY	601
Qy	601	SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV	660
Db	602	 SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV	661
Qy	661	LIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI	720
Db	662	 LIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI	721
Qy	721	FVAACPLAPLFA LLNNWVEIRLDARKEVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	780
Db	722	 FVAACPLAPLFA LLNNWVEIRLDARKEVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	781
Qy	781	AFLLAFFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTCERYAFRDDDGHYS	840

http://es/ScoreAccessWeb/GetItem.action?AppId=10552...4_083145_us-10-552-515-1.rag&ItemType=4&startByte=0 (13 of 44)10/10/2008 8:48:10 AM

activity of a cancer related gene, a method of identifying an anti-neoplastic agent involving contacting a cell exhibiting neoplastic activity with a compound first identified as a cancer related gene modulator using and determining a decrease in neoplastic activity after contacting, when compared to when the contacting does not occur, or administering an agent first identified to an animal exhibiting a cancer condition and detecting a decrease in cancerous condition, a method of determining the cancerous status of a cell involving determining an increase in the level of expression in a cell of a gene where an elevated expression relative to a known non-cancerous cell indicates a cancerous state or potentially cancerous state, an antibody that reacts with a prostate specific polypeptide, an immunoconjugate comprising the antibody and a cytotoxic agent, a method of treating cancer involving contacting a cancerous cell in vivo with an agent having activity against a prostate specific polypeptide and an immunogenic composition the prostate specific polypeptide. The prostate specific polypeptide is useful for identifying an agent that modulates the activity of a cancer related gene. The immunogenic composition is useful for treating cancer, preferably prostate cancer in an animal, e.g. human, which involves administering the immunogenic composition that is sufficient to elicit the production of cytotoxic T lymphocytes specific for the prostate specific polypeptide. The invention is useful for identifying anti-neoplastic agents. This sequence represents a human prostate specific polypeptide of the invention.

XX

SQ Sequence 843 AA;

Query Match 88.2%; Score 4364.5; DB 10; Length 843;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 824; Conservative 0; Mismatches 0; Indels 3; Gaps 2;

Qy	1	MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAERWAMTSETSSGSHCARSRLRRRA	60
Db	5	MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAERWAMTSETSSGSHCA--RMLRRRA	62
Qy	61	QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQQAACRAGSPAKPRIADFLVWWEEDL	120
Db	63	QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQQAACRAGSPAKPRI-DFVLVWWEEDL	121
Qy	121	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLC	180
Db	122	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLC	181
Qy	181	YYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLEVVPDVPPEYYSCRFRVKNLPRF	240
Db	182	YYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLEVVPDVPPEYYSCRFRVKNLPRF	241
Qy	241	LGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT	300

Db	242	LGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPPLHDGPFKT	301
Qy	301	PPEGPQAPRLNQRVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA	360
Db	302	PPEGPQAPRLNQRVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA	361
Qy	361	AVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDH	420
Db	362	AVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDH	421
Qy	421	GGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	480
Db	422	GGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	481
Qy	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVVSRSGNTLLAAW	540
Db	482	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVVSRSGNTLLAAW	541
Qy	541	ASRIASLTGSVNVNLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFY	600
Db	542	ASRIASLTGSVNVNLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFY	601
Qy	601	SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV	660
Db	602	SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV	661
Qy	661	LIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI	720
Db	662	LIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI	721
Qy	721	FVAACPLAPLFAALLNNWVEIRLDARKEVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	780
Db	722	FVAACPLAPLFAALLNNWVEIRLDARKEVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	781
Qy	781	AFLLAFFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTC	827
Db	782	AFLLAFFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTC	828

RESULT 5
ABG15488
ID ABG15488 standard; protein; 898 AA.
XX
AC ABG15488;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #15479.
XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS79675.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 45847; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 898 AA;

Query Match 75.5%; Score 3736; DB 4; Length 898;
Best Local Similarity 82.3%; Pred. No. 0;
Matches 727; Conservative 4; Mismatches 16; Indels 136; Gaps 6;

Qy	1	MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAER-----	37
Db	1	MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAERATDVVLLAPFCQPKTRSHGTCPP	60
Qy	38	-----W---AMTSETS-----SG	47
		:	
Db	61	TERDPRGEGSTEYPGRVDGIQGWGTRALTGWTDRLLCQACQTLPPRHWFLPGARGWLGG	120
Qy	48	SHCA-----RSRMLRRRAQEEDSTVLIDVSPPEAEKRGSYGSTAH	87
		:	
Db	121	SPCAHGQESLPSQPSPILLRVESVKSRLRRRAQEEDSTVLIDVSPPEAEKRGSYGSTAH	180
Qy	88	ASEPGGQQAACRAGSPAKPRIADFLVWEEDLKLDRQQDSAARDRTDMHRTWRETFLDN	147
Db	181	ASEPGGQQAACRAGSPAKPRIADFLVWEEDLKLDRQQDSAARDRTDMHRTWRETFLDN	240
Qy	148	LRAAGLCVDQQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLL	207
		: :	
Db	241	LRAAGLCVDQQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQDYPTRPPTGRPACC	300
Qy	208	AWLGIPNVLLEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTP	267
Db	301	AWLGIPNVLLEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTP	360
Qy	268	YGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWN	327
Db	361	YGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWN	420
Qy	328	KYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGS	387
Db	421	KYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGS	480
Qy	388	KDSFEMCPLCLDCPFWLLSSACALAQ----AGRLFDHGGTVFFSLFMALWAVLLLEYWKR	443
Db	481	KDSFEMCPLCLDCPFWLLSSACALAQVREEAGRLFDHGGTVFFSLFMALWAVLLLEYWKR	540
Qy	444	KSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVV	503
Db	541	KSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVV	600
Qy	504	IVVMVAVVVMCLVSIILYRAIMAIIVVSRSGNTLLAAWASRIASLTGSVNVNLFILILSKI	563

Db	601	IVVMVAVVVMCLVSIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSSVNLVFILILSKI	660
Qy	564	YVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTL	623
Db	661	YVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTL	720
Qy	624	FGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQKFRLRSKKRKAGA	683
Db	721	FGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQKFRLRSKKRKAGA	780
Qy	684	SAGASQGPWEDDYELVPCEGLFDEYLEM-----	711
Db	781	SAGASQGPWEDDYELVPCEGLFDEYLEMGAGFCPNACPELVPPELTEPEKARDQPEARSAG	840
Qy	712	-----VLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKF	747
Db	841	QDSRPEAVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKF	883

RESULT 6

ADB64420

ID	ADB64420 standard; protein; 920 AA.
XX	
AC	ADB64420;
XX	
DT	15-JUN-2007 (revised)
DT	04-DEC-2003 (first entry)
XX	
DE	Human protein encoded by clone FEBRA20031280.
XX	
KW	Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
KW	cell regeneration; membrane protein; signal transduction-related protein;
KW	transcription-related protein; osteoporosis; neurological disease;
KW	cancer; tumour; BOND_PC; transmembrane protein 16D;
KW	transmembrane protein 16D (eight membrane-spanning domains);
KW	transmembrane protein 16D [Homo sapiens]; TMEM16D; FLJ34221; FLJ34272;
KW	FLJ35277; MGC130026; unnamed protein product;
KW	unnamed protein product [Homo sapiens].
XX	
OS	Homo sapiens.
XX	
PN	EP1308459-A2.
XX	
PD	07-MAY-2003.
XX	
PF	28-MAR-2002; 2002EP-00007401.
XX	
PR	05-NOV-2001; 2001JP-00379298.
PR	25-JAN-2002; 2002US-0350978P.

XX
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-450961/43.
DR N-PSDB; ADB62450.
DR PC:NCBI; gi30520318.
XX
PT New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
XX
PS Claim 1; Page; 222pp; English.
XX
CC The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide. The oligonucleotide
CC is useful as a primer for synthesising the polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a protein of the invention. Note: Some of the
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 920 AA;

Query Match 30.9%; Score 1531.5; DB 6; Length 920;

Best Local Similarity 37.9%; Pred. No. 1.1e-147;

Matches 360; Conservative 168; Mismatches 316; Indels 105; Gaps 29;

Qy	44	TSSGSHCARSRMLRRRAQEEDSTVLID---- <td>91</td>	91
		: ::: : : : :	
Db	4	SSSGITNGKTKVFHPVA--KDVNILFDELEAVSSPCKDDDSLHPGNLTSTSDDASRLEA	61
Qy	92	GGQQAACRAGS-----PAKPRIADFLVWEEEDLKLDRQQDSAARDRTDMHRTWRETFLD	146
		: : :: : : : : :	
Db	62	GGETVPERNKSNGLYFRDGKCRI-DYILVYRK-----SNPQTEK----REVFER	105
Qy	147	NLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQE----LPNQASNW	202
		: ::: : : : ::: : :	
Db	106	NIRAEGLQMEKESSLI-NSDII FVKLHAPWEVLGRYAEQMNVRMPFERRKIYYLPRRYKFM	164
Qy	203	S-----AGLLAWLGIPNVLL--EVVPDVPP-EYYSCRFRVKNKLPRFLGSDNQDTFFTST	253
		: : : : : : : : : :: :	
Db	165	SRIDKQISRLRRWLPKKPMRLDKETLPDLEENDCYTAPFSQQRIHHFI-IHNKETFFNNA	223
Qy	254	KRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQ	313
		: : : : :: : :::	
Db	224	TRSRIVHHILQRIKY-EEGKNKIGLNRLLTNGSYEAAFPLHEGSYRSKNSIRTHGAENHR	282
Qy	314	QVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCF	373
		: :: : : :	
Db	283	HLLYECWASWGVWYKYQPLDLVRRYFGEKIGLYFAWLGWYTGMLFPAAFIGLFVFLYGV	342
Qy	374	LVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMAL	432
		: ::: : : : : : : :: :	
Db	343	TLDHSQVSKEVCQATDII-MCPVCDKYCPFMRLSDSCVYAKVTHLFDNGATVFFAVFMAV	401
Qy	433	WAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPER	491
		: : : : : : : : :	
Db	402	WATVFLEFWKRRRAVIAYDWDLIDWEEEEEEIRPQFEAKYSKKERMNPISGKPEPYQAF	461
Qy	492	SRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNTLLA-AWA-----SRIA	545
		: :: : : : : :: : : ::	
Db	462	DKCSRLIVSASGIFFMICVVIAAVFGIVIYRVVTV-----STFAAFKWALIRNNSQVA	514
Qy	546	SLTGSVV--NLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNIFYSSP	603
		: : :: : : : : ::: :: : :	
Db	515	T-TGTAVCINFCIIMLLNVLYEKVALLLTNLEQPRTESEWENSFTLKMFLFQFVNLNSST	573
Qy	604	VYIAFFKGRFVGYPGNYHTLFG--VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLI	662
		: : : : :	
Db	574	FYIAFFLGRFTGHPGAYLRLINRWRLEECHPSGCLIDLQMGIIMVLKQTWNNFMELGY	633
Qy	663	PKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTI	720
		: : : ::: :	

Db	634	PLIQNWWT---RKVRQEHGPERKISFPQWEKDYNLQPMNAYGLFDEYLEMILQFGFTTI	690
Qy	721	FVAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	780
		: :: : : : : : :	
Db	691	FVAAFPLAPLLALLNNIIEIRLDAYKFVTQWRRPLASRAKDIGIWYGILEGIGILSVITN	750
Qy	781	AFLLAFFSSDFLPRAYYRW-----TRAHDLRGFLNFTLA-----RAP	816
		:: : : : : :: :::	
Db	751	AFVIAITSDFIPRLVYAYKYGPCAGQGEAGQKCMVGYNASLSVFRISDFENRSEPESDG	810
Qy	817	SSFAAAHNRTCRYRAFRDDDGH-----YSQTYWNLLAIRLAFVIVFEHVVSFVGRLLDLL	871
		: : : : : :: : : : :	
Db	811	SEFSGTPLKYCRYRDYRDPHSLVPYGYTLQFHWVLAARLAFIIVFEHLVFCIKHLISYL	870
Qy	872	VPDIPESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELSSHW	920
		: : : : :: :: : : : : :	
Db	871	IPDLPKDLRDRMRREKYLIQEMMYEAELERLQKERKERKKNGKAHHNEW	919

RESULT 7

ABP58666

ID	ABP58666	standard; protein; 920 AA.
XX		
AC	ABP58666;	
XX		
DT	24-MAR-2003	(first entry)
XX		
DE	Human	dihydropyrimidinase related protein 1-101.20.
XX		
KW	Human;	dihydropyrimidinase related protein 1-101.20;
KW	recombinant	production; gene therapy; psychosis; development disorder;
KW	uracil-related	metabolic disorder; thymine-related metabolic disorder;
KW	pyrimidine	metabolic disorder.
XX		
OS	Homo sapiens.	
XX		
PN	CN1364894-A.	
XX		
PD	21-AUG-2002.	
XX		
PF	10-JAN-2001;	2001CN-00105195.
XX		
PR	10-JAN-2001;	2001CN-00105195.
XX		
PA	(BIOW-)	BIOWINDOW GENE DEV INC SHANGHAI.
XX		
PI	Mao Y,	Xie Y;
XX		
DR	WPI;	2003-000532/01.

DR N-PSDB; ABZ57080.
XX
PT New polypeptide-human dihydropyrimidinase relative protein 1-101, 20 and
PT polynucleotide for encoding such polypeptide.
XX
PS Claim 1; Page 28-30 (Disclosure); 36pp; Chinese.
XX
CC The invention relates to human dihydropyrimidinase related protein 1-
CC 101.20 (ABP58666) and nucleic acids encoding it (ABZ57080). The protein
CC has a molecular weight of 101.2 kD. The invention also relates to a
CC method for the recombinant production of the protein, an antagonist of
CC the protein, and the use of the protein, gene and antagonist in
CC therapeutic applications. Dihydropyrimidinase related protein 1-101.20
CC can be used in the treatment of a variety of diseases such as psychosis,
CC development disorders and uracil- and thymine-related metabolic
CC disorders. The present sequence represents human dihydropyrimidinase
CC related protein 1-101.20
XX
SQ Sequence 920 AA;

Query Match 30.5%; Score 1511.5; DB 6; Length 920;
Best Local Similarity 37.6%; Pred. No. 1.2e-145;
Matches 357; Conservative 169; Mismatches 318; Indels 105; Gaps 29;

Qy 44 TSSGSHCARSRMLRRRAQEEDSTVLID----VSPPEAE-----KRGSYGST---AHASEP 91
:||| ::: | :| :| | || | : | : || | |
Db 4 SSSGITNGKTKVFHPVA--KDVNILFDELEAVSSPCKDDDSLHPGNLTSTSDDASRLEA 61

Qy 92 GGQQAACRAGS-----PAKPRIADFLVWEEEDLKLDRQQDSAARDRTDMHRTWRETFD 146
||: : | || |::||: : : :|: || |
Db 62 GGETVPERNKSNGLYFRDGKCRI-DYILVYRK-----SNPQTEK----REVFER 105

Qy 147 NLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQE----LPNQASNW 202
|:|| || ::: | : : : | | | || || : :::| : || :
Db 106 NIRAEGLQMEKESSLI-NSDIIFVKLHAPWEVLGRYAEQMNVRMPFRRKIYYLPRRYKFM 164

Qy 203 S-----AGLLAWLGIPNVLL--EVVPDVPP-EYYSRFRVKNLPRFLGSDNQDTFFTST 253
| : || : | | :||: : | : | : : | : |::||| :
Db 165 SRIDKQISRFRRLPKKPMRLDKETLPDLEENDCYTAPFSQQRIHHFI-IHNKETFFNNA 223

Qy 254 KRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQR 313
| :|: || : | | || :|::|| | |||||:| ::: | |
Db 224 TRSRIVHHILQRIKY-EEGKNKIGLNRLLTNGSYEAAFPPLHEGSYRSKNSIRTHGAENHR 282

Qy 314 QVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCF 373
:|:: || || | ||||| |||||: |||||: || | ||| :| ||| |
Db 283 HLLYECWASWGVVYKYQPLDLVRRYFGEKIGLYFAWLGWYTGMFLPAAFIFGLFVFLYGV 342

Qy 374 LVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMAL 432

Db	343	TLDHSQVSKEVCQATDII-MCPVCDKYCPFMRLSDSCVYAKVTHLFDNGATVFFAVFMAV	401
Qy	433	WAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPER	491
Db	402	WATVFLEFWKRRRAVIAYDWDLIDWEEEEEEIRPQFEAKYSKKERMNPISGKPEPYQAFT	461
Qy	492	SRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNTLLA-AWA-----SRIA	545
Db	462	DKCSRLIVSASGIFFMICVVIAAVFGIVIYRVVTV-----STFAAFKWALIRNNSQVA	514
Qy	546	SLTGSVV--NLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSP	603
Db	515	T-TGTAVCINFCCIIMLLNVLYEKVALLLTNLEQPRTESEWENSFTLKMFLFQFVNLNSST	573
Qy	604	VYIAFFKGRFVGYPGNYHTLFG-VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLI	662
Db	574	FYIAFFLGRFTGHPGAYLRLINRWRLEECHPSGCLIDLQMGIIMVLKQTNWNFMELGY	633
Qy	663	PKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTI	720
Db	634	PLIQNWWTR---RKVRQEHGPERKISFPQWEKDYNLQPMNAYGLYDEYLEMILQFGFTTI	690
Qy	721	FVAACPLAPLFPALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	780
Db	691	FVAAFPLAPLLALLNNIIEIRLDAYKFVTQWRRPLASRAKDIGIGYGILEGIGILSVITN	750
Qy	781	AFLLAFFSSDFLPRAYRW-----TRAHDLRGFLNFTLA-----RAP	816
Db	751	AFVIAITSDFIPRLVYAYKYGPCAGQGEAGQKCMVGYNASLSVFRISDFENRSEPESDG	810
Qy	817	SSFAAAHNRTCRYRAFRDDDGH-----YSQTYWNLLAIRLAFVIVFEHVVSFVGRLDLL	871
Db	811	SEFSGTPLKYCRYRDYRDPHSLVPYGYTLQFWHVLAARLAFIIVFEHLVFCIKHLISYL	870
Qy	872	VPDIPESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELSSHW	920
Db	871	IPDLPKDLRDRMRREKYLIQEMMYEAELERLQKERKERKKNGKAHHNEW	919

RESULT 8
ADK52114
ID ADK52114 standard; protein; 981 AA.
XX
AC ADK52114;
XX
DT 15-JUN-2007 (revised)
DT 20-MAY-2004 (first entry)
XX

DE Human atopic dermatitis/psoriasis-associated protein #29.
XX
KW Human; atopic dermatitis; psoriasis; dermatological; anti-inflammatory;
KW antipsoriatic; rash; BOND_PC; transmembrane protein 16C;
KW chromosome 11 open reading frame 25;
KW transmembrane protein 16C [Homo sapiens]; TMEM16C; C11orf25; GENX-3947;
KW transmembrane protein 16C (eight membrane-spanning domains);
KW hypothetical protein; hypothetical protein [Homo sapiens]; GO16020;
KW GO16021; GO4185; GO7001.
XX
OS Homo sapiens.
XX
PN WO2004016785-A1.
XX
PD 26-FEB-2004.
XX
PF 06-AUG-2003; 2003WO-JP009999.
XX
PR 06-AUG-2002; 2002JP-00229319.
PR 14-MAY-2003; 2003JP-00136544.
XX
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
XX
PI Itoh M, Ogawa K, Shinagawa A, Sudo H, Ogawa H, Ra C;
PI Mitsuishi K;
XX
DR WPI; 2004-214514/20.
DR N-PSDB; ADK52028.
DR PC:NCBI; gi13899227.
DR PC:SWISSPROT; Q9BYT9.
XX
PT Detecting atopic dermatitis or psoriasis comprises assaying levels of
PT expression of an indicator gene at a rash site and non-rash site of a
PT person with atopic dermatitis or psoriasis.
XX
PS Example 2; SEQ ID NO 147; 484pp; Japanese.
XX
CC The invention relates to detecting atopic dermatitis or psoriasis
CC comprising assaying the levels of expression of an indicator gene at a
CC rash site and non-rash site of a person with atopic dermatitis or
CC psoriasis, comparing these levels with those of a healthy person, and
CC determining that if the levels of indicators are higher or lower, then
CC this indicates the disease. Also included are a reagent for detecting
CC atopic dermatitis or psoriasis, a kit for screening for treatments, a
CC transgenic non human vertebrate animal models for the diseases, an agent
CC for inducing the diseases in mice and a DNA chip for assaying for the
CC indicator genes. The method is used for treatment, detection and animal
CC models for research of atopic dermatitis and psoriasis. The present

CC sequence is a protein encoded by an indicator gene of the invention.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 981 AA;

Query Match 30.4%; Score 1504; DB 8; Length 981;
Best Local Similarity 39.4%; Pred. No. 8.1e-145;
Matches 329; Conservative 163; Mismatches 268; Indels 76; Gaps 24;

Qy	106	KPRIADFVLVWEEDLKLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNT	165
		: : : :: :::: :	
Db	161	KRRI-DYILVYR-----KTNIPYDKRNTFEKNLRAEGLMLEKEPA-IASP	203
Qy	166	TVHYALLSASWAVLCYYAEDLRLKLPLQ-----ELPNQASNWSAGLLAWLGIPNV	215
		: : : : : : : : : : : :	
Db	204	DIMFIKIHIPWDTLCKYAERLNIRMPFRKKCYITDGRSKSMGRMQTYFRIKDWMAQNPM	263
Qy	216	LLE--VVPDV-PPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPY--GH	270
		: : : : : :: : : : : : : : : : : :	
Db	264	VLDKSAFPDLEESDCYTGPFSRARIHHFI-INNKDTFFSNATRSRIVYHMLERTKYENGI	322
Qy	271	EKKNLLGIHQLLAEGVLSAAFPLHDGPFKT---PPEGPQAPRLNQRVLFQHWARWGKW	326
		: : : : : : :	
Db	323	SK---VGIRKLINNGSYIAAFPPEHAGYKSSQPIKTHGPQ---NNRHLLYERWARWGMW	375
Qy	327	NKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCG	386
		: : : : : : : : : : : :	
Db	376	YKHQPLDLIRLYFGEKIGLYFAWLGWYTGMILPAAIVGLCVFFYGLFTMNSQVSQEICK	435
Qy	387	SKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKS	445
		: : : : : : : : : : : : : : : :	
Db	436	ATEVF-MCPLCDKNCSLQRLNDSCIYAKVTYLFDNGGTVFFAIFMAIWATVFLFWKRRR	494
Qy	446	ATLAYRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSVVI	504
		: : : : : : : :	
Db	495	SILTYTWDLIEWEEEEETLRPQFEAKYYKMEIVNPITGKPEPHQPS SDKVTRLLVSVSGI	554
Qy	505	VVMVAVVVMCLVSIILYR-AIMAIVVSRSGNTLLAAWASRIASLTGSV-VNLVFILILSK	562
		:: : : ::: : : : : : : : : :	
Db	555	FFMISLVITAVFGVVYRLVMEQFASFKNFIKQYW--QFATSAAAVCINFIIIMLLNL	612
Qy	563	IYVSLAHVLTWRWEMHRTQTKFEDAFTLKVFIFQFVNFIYSSPVYIAFFKGRFVGYPGNYHT	622
		: : : ::: : : : : : :	
Db	613	AYEKIAYLLTNLEYPRTESEWENSFALKMFLFQFVNLNSSIFYIAFFLGRFVGHPGKYNK	672
Qy	623	LFG-VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLPKLGWWQKFRLRSKKRKA	681
		: : : : : : : : :	

AEN06206

XX

XX

DT 22-FEB-2007 (first entry)

XX

XX

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XX

XX

XX

XX

http://es/ScoreAccessWeb/GetItem.action?AppId=10552...4_083145_us-10-552-515-1.rag&ItemType=4&startByte=0 (26 of 44)10/10/2008 8:48:10 AM

Qy	166	TVHYALLSASWAVLCYYAEDLRLKLPLQ-----ELPNQASNWSAGLLAWLGIPNV	215
Db	204	DIMFIKIHIPWDTLCKYAERLNIRMPFRKKCYITDGRSKSMGRMQTYFRRIKDWMAQNPM	263
Qy	216	LLE--VVPDV-PPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPY--GH	270
Db	264	VLDKSAFPDLEESDCYTGPFSRARIHFFI-INNKDTFFSNATRSRIVYHMLERTKYENGI	322
Qy	271	EKKNLLGIHQLLAEGVLSAAFPLHDGPFKT---PPEGPQAPRLNQQRQVLFQHWARWGKW	326
Db	323	SK---VGIRKLINNGSYIAAFPPEHAGAYKSSQPIKTHGPQ---NNRHLLYERWARWGMW	375
Qy	327	NKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCG	386
Db	376	YKHQPLDLIRLYFGEKIGLYFAWLGWYTGMLIPAAIVGLCVFFYGLFTMNNSQVSQEICK	435
Qy	387	SKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKS	445
Db	436	ATEVF-MCPLCDKNCSLQRLNDSCIYAKVTYLFDNNGGTVFFAIFMAIWATVFLEFWKRRR	494
Qy	446	ATLAYRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSVVI	504
Db	495	SILTYTWDLIEWEEEEETLRPQFEAKYYKMEIVNPITGKPEPHQPSSDKVTRLLVSVSGI	554
Qy	505	VVMVAVVVMCLVSIILYR-AIMAIVVSRSGNTLLAAWASRIASLTGSV-VNLVFILILSK	562
Db	555	FFMISLVITAVFGVVYRLVVMEQFASFKNFIKQYW--QFATSAAAVCINFIIIMLLNL	612
Qy	563	IYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHT	622
Db	613	AYEKIAYLLTNLEYPRTESEWENSFALKMFLFQFVNLNSSIFYIAFFLGRFVGHPGKYNK	672
Qy	623	LFG-VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLPKLGWWQKFRLRSKKRKA	681
Db	673	LFDRWRLEECHPSGCLIDLCLQMGVIMFLKQIWNNFMELGYPLIQNWWSRHKI-----KR	727
Qy	682	GASAGASQGPWEDDYELVP--CEGLFDEYLEMVLQFGFVTIFVAACPLAPLFAALLNNWVE	739
Db	728	GIH-DASIPQWENDWNLQPMNLHGLMDEYLEMVLQFGFTTIFVAAPLAPLLALLNNIIE	786
Qy	740	IRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRW-	798
Db	787	IRLDAYKFVTQWRRPLPARATDIGIWLGILEGIGILAVITNAFVIAITSYIPRFVYEEK	846
Qy	799	-----TRAHDLRGFLNFTTLARAP-SSFAAAHNRTCryRAFR-----DDDGHSQTY	843
Db	847	YGPCANHVEPSENCLKGYVNNLSFFDLSELGMGKSGYCRYRDYRGPPWSSKPYEFTLQY	906
Qy	844	WNLLAIRLAFVIVFEHVVSFVGRLDLLVDPDIPESVEIKVKREYYLAKQALAENEV	899

Db 907 WHILAARLAFIIVFEHLVFGIKSFIAYLIPDVPKGLHDIRREKYLQEMMYEAEEL 962

RESULT 10

AFB77190

ID AFB77190 standard; protein; 1017 AA.

XX

AC AFB77190;

XX

DT 28-JUN-2007 (first entry)

XX

DE Mouse TM-1 (Tmem16a) protein.

XX

KW Cell isolation; stem cell; therapeutic; transgenic animal; screening;

KW tissue regeneration; genitourinary disease; uropathic;

KW intervertebral disk displacement; degeneration; injury; vulnerary;

KW back pain; transmembrane factor-1; Tmem16a.

XX

OS Mus musculus.

XX

PN WO2007027583-A2.

XX

PD 08-MAR-2007.

XX

PF 28-AUG-2006; 2006WO-US033491.

XX

PR 31-AUG-2005; 2005US-0713400P.

XX

PA (UYFL) UNIV FLORIDA RES FOUND INC.

XX

PI Harfe BD, Cohn MJ;

XX

DR WPI; 2007-412931/39.

DR N-PSDB; AFB77189.

XX

PT Isolating sonic hedgehog expressing-cells comprises obtaining a non-human

PT transgenic subject in which a marker gene has been inserted into the

PT subject's genome.

XX

PS Disclosure; SEQ ID NO 2; 96pp; English.

XX

CC The present invention relates to a method of isolating cells in selected
 CC tissues co-expressing the sonic hedgehog (Shh) gene and a marker gene.

CC The method involves obtaining a non-human transgenic subject in which a
 CC marker gene has been inserted into the subject's genome and isolating

CC Shh/marker gene expressing cells and Shh/marker gene non-expressing cells
 CC from the selected tissue. The invention further provides a method of

CC identifying differentially expressed genes (e.g. transmembrane factors TM

CC -1 and TM-2, EST 1437418, Mmu-miR-135a-2 and AP-2 beta) in selected
 CC tissues co-expressing the sonic hedgehog gene and a marker gene. The
 CC invention is useful in tissue engineering, regeneration, reconstruction
 CC and/or repair of tissues and genitourinary system and also in treating
 CC intervertebral disk rupture, degeneration, disease or injury and back
 CC pain. The invention is further useful for generating transgenic animal.
 CC The present sequence is the mouse TM-1 (Tmem16a) protein.

XX

SQ Sequence 1017 AA;

Query Match 30.1%; Score 1489; DB 12; Length 1017;
 Best Local Similarity 37.5%; Pred. No. 3e-143;
 Matches 361; Conservative 170; Mismatches 303; Indels 128; Gaps 29;

Qy 26 GLYCRDQAHAERWAMT--SETSSGSHCARSRMLRRRAQEEDSTVLIDVSPPEAEKRGSYG 83
 ||| || : : : :|| || | || : | : |:
 Db 109 GLYFRDQKRGKVDYILVYHHKRASG-----SRTLARRGLQNDMVL-----GTRS 151

Qy 84 STAHASEPGGQQAACRAGSPAKPRIADFLVWEEDLKLDRQQDSAARDRTDMHRTWRET 143
 || : : |||| | :| :| | ||
 Db 152 VRQDQPLPG--KGSPVDAGSPEVP-----MDYHEDD-----KRFRREE 187

Qy 144 FLDNLRAAGLCVDQQDVQDGNTTVH---YALLSASWAVLCYYAEDLRLKLPLQELPNQAS 200
 : || ||| :: | :| :| : : | | || | | :||:| :: : :
 Db 188 YEGNLLLEAGLELE---NDEDTKIHGVGFVKIHAPWHVLCREAEFLKLKMPTKKVYHISE 243

Qy 201 NWSAGLLAWLGIPNVLLEVVPDVPPEYYSCRFRVNKLPRFLGS-----DNQDTFFT 251
 : ||| | :|| :: : |: | : | :| :||:|
 Db 244 --TRGLLK--TINSVLQKITDPIQPKVAEHRPQTTKRLSYFFSREKQHLFDLTDRDSFFD 299

Qy 252 STKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFLPHDGPFKTPPEGPQAPRLN 311
 | | |::||| :| | : :|| ||| || |||:|||| : || |
 Db 300 SKTRSTIVYEILKRTTCTKAKYS-MGITSLLANGVYSAAYPLHDGDY---EGDNV-EFN 353

Qy 312 QRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVG 371
 |::|:: || :| : ||||:| ||:||||| ||||| || |::|::|| :||| |
 Db 354 DRKLLYEEWASYGVFYKYQPIDLVRKYFGEKVGLYFAWLGAYTQMLIPASIVGVIVFLYG 413

Qy 372 CFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFM 430
 | | :||: |:| : : |||| | :| :|||| |:| |||: ||||:|
 Db 414 CATVDENIPSMEMCDQRYNITMCPLCDKTCYWKMSACATARASHLFDNPATVFFSVFM 473

Qy 431 ALWAVLLLEYWKRKSATLAYRWDCSDYEDTEE----RPRPQFAA----SAPMTAPNPIT 481
 |||| :|:|||| | |||| : :|| || | : : | :| |
 Db 474 ALWAATFMEHWKRKQMLNRYRWDLTGFEETEEAVKDHPRAEYEARVLEKSLRKESRNKET 533

Qy 482 GEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVVSRSGNTLLAAWA 541
 |: | | | |:|:| : : :||| | : : : : : :
 Db 534 --DKVKLTWRDRFPAYFTNLVSIIFMIAVTFAIVLGVIIYRISTAAALAMNSSPSVRSNI 591

Qy	542	SRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYS	601
		: : : : : : : : : : : : :	
Db	592	RVTVTATAVIINLVIIILLDEVYGC IARWLTKIEVPKTEKSFEERLTFKAFL LKFVNSYT	651
Qy	602	SPVYIAFFKGRFVGYPGNYHTLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI-NNMQE	659
		: : : : : : : : :	
Db	652	PIFYVAFFKGRFVGRPGDYVYIFRSFRMEECAPGGCLMELCIQLSIIMLGKQLIQNNLFE	711
Qy	660	VLIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVT	719
		: : : : : : : : : : : :	
Db	712	IGIPKMKKFIRYLKLRRQSPSDREEYVKRKQRYEVDNFLEPFAGLTPEYMEMIIQFGFVT	771
Qy	720	IFVAACPLAPL FALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVIS	779
		: : : : :	
Db	772	LFVASFPLAPL FALLNNIIEIRLDAKKFVTELRRPV AIRAKDIGI WYNILRGVGKLAVII	831
Qy	780	NAFL LAFSSDFLPRAYYRWTRAHD--LRGFLNFTLARAPSSF-----AAAHN-----	824
		: : : : : : : :	
Db	832	NAFVISFTSDFIPRLVYLYMYSQNGTMHGFVNHTL----SSFNVSDFQNGTAPNDPLDLG	887
Qy	825	---RTC RYAFRD---DDGHY--SQTYWNLLAIRLAFVIVFEHV VFSVGRLLDLLVPDIP	876
		: : : : : : : : : : : :	
Db	888	YEVQICRYKDYREPPWSEHKYDISKDFWAVLAARLAFVIVFQNLVMFMSDFVDWVIPDIP	947
Qy	877	ESVEIKVKREYYL-----AKQALAE NEVLFGTNGTKDEQPKGSELSSHWPFTVP	926
		: : : : : : : : : : : : : :	
Db	948	KDISQQIHKEKVL MVELFMREEQGKQQLLDTWM-----EKEKPRDVPCNNH-SPTTHP	999
Qy	927	KA	928
		:	
Db	1000	EA	1001

RESULT 11
AEG11142
ID AEG11142 standard; protein; 960 AA.
XX
AC AEG11142;
XX
DT 15-JUN-2007 (revised)
DT 20-APR-2006 (first entry)
XX
DE Human transmembrane protein 16A, SEQ ID NO: 7.
XX
KW Genetic marker; diagnostic; prognosis; gastrointestinal tumor;
KW cytostatic; neoplasm; tumor marker; transmembrane protein 16A; BOND_PC;
KW transmembrane protein 16A;
KW transmembrane protein 16A (eight membrane-spanning domains);

KW oral cancer overexpressed 2; membrane protein;
KW tumor amplified and overexpressed sequence 2;
KW transmembrane protein 16A [Homo sapiens]; TMEM16A; TAOS2; ORAOV2;
KW FLJ10261.
XX
OS Homo sapiens.
XX
PN US2006040292-A1.
XX
PD 23-FEB-2006.
XX
PF 08-JUL-2005; 2005US-00177894.
XX
PR 08-JUL-2004; 2004US-0586676P.
XX
PA (WEST/) WEST R B.
PA (VRIJ/) VAN DE RIJN M.
XX
PI West RB, Van De Rijn M;
XX
DR WPI; 2006-182760/19.
DR N-PSDB; AEG11136.
DR REFSEQ; NP_060513.
DR PC:NCBI; gi40354210.
XX
PT Classifying tumor as gastrointestinal stromal tumor belonging to PDGFRA
PT positive subclass, involves detecting expression or activity of gene
PT encoding DOG1 polypeptide in sample.
XX
PS Disclosure; SEQ ID NO 7; 177pp; English.
XX
CC The present invention relates to three gene markers such as DOG1, KIT and
CC platelet derived-growth factor receptor alpha (PDGFRA) that are useful in
CC classifying tumors. These gene markers are useful in the classification
CC of gastrointestinal stromal tumors (GISTs) and tumors other than GISTs.
CC The invention also relates to methods providing diagnostic, prognostic
CC and predicative information based on the classifying step. The invention
CC is useful for classifying gastrointestinal stromal tumors as belonging to
CC a PDGFRA positive subclass, KIT negative or PDGFRA negative subclass. The
CC present sequence is human transmembrane protein 16A (DOG1; TMEM16A). The
CC DOG1 gene encodes a transmembrane protein of unknown function
CC (transmembrane protein 16A). The transmembrane protein 16A is encoded by
CC DOG1 gene that is mapped to 11q13.2 on chromosome 11.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 960 AA;

Query Match 30.1%; Score 1488; DB 11; Length 960;
 Best Local Similarity 37.6%; Pred. No. 3.5e-143;
 Matches 363; Conservative 160; Mismatches 307; Indels 136; Gaps 28;

Qy	26	GLYCRDQAHAERWAMT--SETSSGSHCARSRMLRRRAQEEDSTVLIDVSPPEAEKRGSYG	83
		: : : : :	
Db	52	GLYFRDGRRKVDYILVYHHKRPSG-----NRTLVRVQHS DTP-----SGA	92
Qy	84	STAHASEPGGQQAACRAGSPAKPRIADFLVWEEDLKLDRQQDSAARDRTDMHRTWRET	143
		: : : : :	
Db	93	RSVKQDHPLPGKGASLDAGSGEPP-----MDYHEDD-----KRFRREE	130
Qy	144	FLDNLRAAGLCVDQQDVQDGNTTVH---YALLSASWAVLCYYAEDLRLKLPLQELPNQAS	200
		: :: : : : : : : : : :: :	
Db	131	YEGNLLEAGLELE---RDEDTKIHGVGFVKIHAPWNVLCREAEFLKLKMPTKKMYH--I	184
Qy	201	NWSAGLLAWLGIPNVLLEVVPDVPPEYYSCR-----FRVNKLPRFLGSDNQDTFF	250
		: : :: : : : :	
Db	185	NETRGLLK--KINSVLQKITDPIQPKVAEHRPQTMKRLSYPFSSREKQHLFDLSD-KDSFF	241
Qy	251	TSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRL	310
		:: : : : : : : :	
Db	242	DSKTRSTIVYEILKRTTCTKAKYS-MGITSLLANGVYAAAYPLHDGDY-----NGENVEF	295
Qy	311	NQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLV	370
		:: :: : : : : : : : : :	
Db	296	NDRKLLYEEWARYGVFYKYQPIDLVRKYFGEKIGLYFAWLGVYTQMLIPASIVGIIVFLY	355
Qy	371	GCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLF	429
		: : : : : : : : : : :	
Db	356	GCATMDENIPSMEMCDQRHNITMCPLCDKTC SYWKMS SACATARASHLFDNPATVFFSVF	415
Qy	430	MALWAVLLLEYWKRKSATLAYRWDCSDYEDTEE---RPRPQFAA-----SAPMTAPNPI	480
		: : : : : : : :	
Db	416	MALWAATFMEHWKRKQMRNLNYRWDLTGFEETEEEAVKDHPRAEYEAREVLEKSLKKESRKE	475
Qy	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVVSRSGNTLLAAW	540
		: : : :: : : : : : : :	
Db	476	T--DKVKLTWRDRFPAYLTNLVSIIFMIAVTFAIVLGVIIRISMAAALAMNSSPSVRSN	533
Qy	541	ASRIASLTGSVNVLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFY	600
		: : :: :: : : : : : : : :	
Db	534	IRVTVTATAVIINLVVIILLDEVYGC IARWLT KIEVPKTEKSFEERLIFKAFLK FVNSY	593
Qy	601	SSPVYIAFFFKGRFVGYPGNYHTLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI--NNMQ	658
		: : : : : : : : : :	
Db	594	TPIFYVAFFFKGRFVGRPGDYVYIFRSFRMEECAPGGCLMELCIQLSIIMLGKQLIQNNLF	653
Qy	659	EVLIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFV	718

Db	654	EIGIPKMKKLIRYLKLKQQSPPDHEECVKRKQRYEVDYNLEPFAGLTPEYMEMIIQFGFV	713
Qy	719	TIFVAACPLAPLFFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVI	778
Db	714	TLFVASFPLAPLFFALLNNIEIRLDAKKFVTELRRPVAVRAKDIGIWYNILRGIGKLAVI	773
Qy	779	SNAFLLAFFSSDFLPRA--YYRWTRAHDLRGFLNFTLARAPSSF-----AAAHN-----	824
Db	774	INAFVISFTSDFIPRLVYLYMYSKNGTMHGFVNHTL----SSFNVSDFQNGTAPNDPLDL	829
Qy	825	----RTCRYRAFRD---DDGHY--SQTYWNLLAIRLAFVIVFEHVVFVSVGRLLDLLVPDI	875
Db	830	GYEVQICRYKDYREPPWSENKYDISKDFWAVLAARLAFVIVFQNLVMFMSDFVDWVIPDI	889
Qy	876	PESVEIKVKREYYLA-----KQALAENEVLFGTNGTKDEQP-----KG	913
Db	890	PKDISQQIHKEKVLMLVELFMREEQDKQQLL--ETWMEKERQKDEPPCNHHNTKACPDSLG	947
Qy	914	SELSSH	919
Db	948	SPAPSH	953

RESULT 12

AEG11146

ID	AEG11146	standard; protein; 840 AA.
XX		
AC	AEG11146;	
XX		
DT	15-JUN-2007	(revised)
DT	20-APR-2006	(first entry)
XX		
DE	Human transmembrane protein 16A,	SEQ ID NO: 11.
XX		
KW	Genetic marker; diagnostic; prognosis; gastrointestinal tumor;	
KW	cytostatic; neoplasm; tumor marker; transmembrane protein 16A; BOND_PC;	
KW	TMEM16A protein; TMEM16A protein [Homo sapiens].	
XX		
OS	Homo sapiens.	
XX		
PN	US2006040292-A1.	
XX		
PD	23-FEB-2006.	
XX		
PF	08-JUL-2005; 2005US-00177894.	
XX		
PR	08-JUL-2004; 2004US-0586676P.	
XX		

PA (WEST/) WEST R B.
PA (VRIJ/) VAN DE RIJN M.
XX
PI West RB, Van De Rijn M;
XX
DR WPI; 2006-182760/19.
DR N-PSDB; AEG11141.
DR GENBANK; AAH33036.
DR PC:NCBI; gi34192278.
XX
PT Classifying tumor as gastrointestinal stromal tumor belonging to PDGFRA
PT positive subclass, involves detecting expression or activity of gene
PT encoding DOG1 polypeptide in sample.
XX
PS Disclosure; SEQ ID NO 11; 177pp; English.
XX
CC The present invention relates to three gene markers such as DOG1, KIT and
CC platelet derived-growth factor receptor alpha (PDGFRA) that are useful in
CC classifying tumors. These gene markers are useful in the classification
CC of gastrointestinal stromal tumors (GISTs) and tumors other than GISTs.
CC The invention also relates to methods providing diagnostic, prognostic
CC and predicative information based on the classifying step. The invention
CC is useful for classifying gastrointestinal stromal tumors as belonging to
CC a PDGFRA positive subclass, KIT negative or PDGFRA negative subclass. The
CC present sequence is human transmembrane protein 16A (DOG1; TMEM16A). The
CC DOG1 gene encodes a transmembrane protein of unknown function
CC (transmembrane protein 16A). The transmembrane protein 16A is encoded by
CC DOG1 gene that is mapped to 11q13.2 on chromosome 11.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 840 AA;

Query Match 29.9%; Score 1479.5; DB 11; Length 840;
Best Local Similarity 40.0%; Pred. No. 2.2e-142;
Matches 340; Conservative 152; Mismatches 270; Indels 89; Gaps 22;

Qy 135 DMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVH---YALLSASWAVLCYYAEDLRLKLP 191
| | || : || ||| :: :| :| :| : : | | ||| || |:|:|
Db 6 DDKRFRREEYEGNLLLEAGLELE----RDEDTKIHGVGFVKIHAPWNVLCREAEFLKCLKMP 61

Qy 192 LQELPNQASNWSAGLLAWLGIPNVLLLEVVPDVPPEYYSCR-----FRVKNKLPRFL 241
::: : | : ||| | :|| :: : |: | | | |
Db 62 TKKMYH--INETRGLLK--KINSVLQKITDPIQPKVAEHRPQTMKRLSYPFSSREKQHLFD 117

Qy 242 GSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTP 301
|| :|:| | | | :|:| | :| :| | | | | :|:|:|:|:| :
Db 118 LSD-KDSFFDSKTRSTIVYEILKRTTCTKAKYS-MGITSLLANGVYAAAYPLHDGDY--- 172

Qy	302	PEGPQAPRLNQQRQLFQHVARWGKWNKYQPLDHVRRYFGGEKVALYFAWLGFYTGWLLPAA	361
		: : :: : : : : : : :	
Db	173	--NGENVEFNDRKLLYEWEARYGVFYKYQPIDLVRKYFGEKIGLYFAWLGVTYQMLIPAS	230
Qy	362	VVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFHDH	420
		: : : : : : : : : : : :	
Db	231	IVGIIVFLYGCAITMDENIPSMEMCDQRHNITMCPLCDKTCSYWKMSSACATARASHLFDN	290
Qy	421	GGTVFFSLFMALWAVLLLEYWKRSATLAYRWDCSDYEDTEERPRPQFAA-----SAPMT	475
		: : : : : : : ::	
Db	291	PATVFFSVFMALWAATFMEHWKRKQMRLNYRWDLTGFEEDDHPRAEYEARVLEKSLKKE	350
Qy	476	APNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNT	535
		: : : : :: : : :: :	
Db	351	SRNKET--DKVKLTWRDRFPAYLTNLVSIIFMIAVTFAIVLGVIIYRISMAAALAMNSSP	408
Qy	536	LLAAWASRIASLTGSVNVLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQ	595
		: : : :: : :: : : : : : : : :	
Db	409	SVRSNIRVTVTATAVIINLVVIIILLDEVYGCARWLTKEVPKTEKSFEERLIFKAFLK	468
Qy	596	FVNFIYSSPVYIAFFFKGRFVGYPGNYHTLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI	654
		: : : : : : : : : :	
Db	469	FVNSYTPIFYVAFFFKGRFVGRPGDYVYIFRSFRMEECAPGGCLMELCIQLSIIMLGKQLI	528
Qy	655	-NNMQEVLIPKLKGWWQKFRLRSKKRKAGASAGASQGPDWEDDYELVPCGLFDEYLEMVL	713
		: : : : : : : : : : :~	
Db	529	QNNLFEIGIPKMKKLIRYLKLKQQSPDHEECVKRKQRYEVDYNLEPFAGLTPEYMEMII	588
Qy	714	QFGFVTIFVAACPLAPLRFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWPHILAGLT	773
		: : : : : : : : : :~ :	
Db	589	QFGFVTILFVASFPLAPLRFALLNNIEIRLDAKKFVTELRRPVAVRAKDIGIWINLRGIG	648
Qy	774	HIAVISNAFLAFSSDFLPRA--YYRWTRAHDLRGFLNFTLARAPSSF-----AAAHN	824
		: :~::~ : : :~: : :	
Db	649	KLAVIDADFVISFTSDFIPRLVLYLMYSKNGTMHGTFVNHTL----SSFNVSDFQNGTAPN	704
Qy	825	-----RTCERYAFRD---DDGHY--SQTYWNLLAIRLAFVIVFEHVVSFVGRLLDL	870
		: : : : : : : : :~:~ : :	
Db	705	DPLDLGYEVQICRYKDYREPPWSENKYDISKDFWAVLAARLAFVIVFQNLMFMMSDFVDW	764
Qy	871	LVPDIPESVEIKVKREYYLA-----KQALAENEVLFGTNGTKDEQP-----	911
		:~ : :~: : ~:~:~	
Db	765	VIPDIPKDISQQIHKEKVLMMVELFMREEQDKQQLL--ETCMEKERQKDEPPCNHHNTKAC	822
Qy	912	---KGSELSSH 919	
Db	823	PDSLGPAPSH 833	

RESULT 13

ADG48280

ID ADG48280 standard; protein; 1003 AA.

XX

AC ADG48280;

XX

DT 11-MAR-2004 (first entry)

XX

DE Human retina-specific protein - C12orf3variants.

XX

KW human; retina-specific protein; NET01; retinal disease;

KW age related macular degeneration; night blindness; C12orf3variants.

XX

OS Homo sapiens.

XX

PN WO2003068967-A2.

XX

PD 21-AUG-2003.

XX

PF 18-FEB-2003; 2003WO-EP001625.

XX

PR 18-FEB-2002; 2002EP-00003675.

PR 21-FEB-2002; 2002US-0357857P.

XX

PA (LYNK-) LYNKEUS BIO TECH GMBH.

XX

PI Stoehr BH, Weber FHB, Goehring F;

XX

DR WPI; 2003-767334/72.

DR N-PSDB; ADG48279.

XX

PT New nucleic acid encoding retinal protein sNET01, useful for diagnosis of
PT retinal disease, especially macular degeneration, also for drug screening
PT and therapy.

XX

PS Claim 18; Fig 14; 199pp; English.

XX

CC The invention comprises the amino acid and coding sequences of a human
CC retina-specific protein - NET01. The DNA and protein sequences of the
CC invention are useful in the treatment of retinal diseases, such as
CC macular degeneration (especially age related) and night blindness. The
CC present amino acid sequence represents the human retina-specific protein
CC C12orf3variants.

XX

SQ Sequence 1003 AA;

Query Match 29.6%; Score 1464; DB 7; Length 1003;

Best Local Similarity 37.4%; Pred. No. 1.1e-140;

http://es/ScoreAccessWeb/GetItem.action?AppId=10552...4_083145_us-10-552-515-1.rag&ItemType=4&startByte=0 (38 of 44)10/10/2008 8:48:10 AM

Qy 758 RAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYRWTRAHD--LRGFLNFTLA-- 813
| :||||| ||:| : |||||::| :|||:| |:: :| : ||:| ||:
Db 796 RTKDIGIWF DILSGIGKFSVISNAFVIAITSDFIPRLVYQYSYSHNGTLHGFEVNHTLSFF 855

Qy 814 -----RAPSSFAAAHNRTCryRAFRD-----DDGHYSQTYWNLLAIRLAFVIVFEH 859
: :| : ||:: :| : :|: || :|: |||||:|::
Db 856 NVSQLKEGTQPEN SQFDQEVQFCRFKDYREPPWAPNPYEF SKQYWFILSARLAFV IIFQN 915

Qy 860 VVFSVGRLDLLVDPDIPESVEIKVKRE-----YYLAKQALAENEVLFGTNGTKDEQPKG 913
:| : |:| ::|||| : ::|| : :| : |:| | : | |
Db 916 LVMFSLVLDVDMIPDIPTDISDQIKKEKSLLVDFFLKE---EHEKLKLMDEPALRSPGG 971

Qy 914 SELSSHWTPTVTPKA-SQL 931
: | : | ||
Db 972 GDRSR SRAASSAPSGQSQL 990

RESULT 14

AEH82071

ID AEH82071 standard; protein; 913 AA.

XX

AC AEH82071;

XX

DT 15-JUN-2007 (revised)

DT 13-JUL-2006 (first entry)

XX

DE Human gnathodiaphyseal dysplasia protein, GDD1.

XX

KW Osteopathic; Gene therapy; bone disease; bone injury; bone resorption;

KW gnathodiaphyseal dysplasia; GDD1; BOND_PC; transmembrane protein 16E;

KW integral membrane protein GDD1; transmembrane protein 16E [Homo sapiens];

KW TMEM16E; GDD1; integral membrane protein GDD1 [Homo sapiens]; G05783;

KW G016020; G016021.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	Inhibitory-site	356
FT		/note= "Missense mutations in the coding sequence can
FT		lead to substitution of this residue with either Arg or
FT		Gly"
XX		
PN	JP2006121961-A.	
XX		
PD	18-MAY-2006.	
XX		
PF	28-OCT-2004; 2004JP-00313511.	
XX		

PR 28-OCT-2004; 2004JP-00313511.
XX
PA (UYTO-) UNIV TOKUSHIMA NAT UNIV CORP.
XX
PI Itakura M, Tsutsumi S, Kamata N, Inoue H;
XX
DR WPI; 2006-367194/38.
DR N-PSDB; AEH82070.
DR PC:NCBI; gi47106048.
DR PC:SWISSPROT; Q75V66.
XX
PT Novel gnathodiaphseal dysplasia DNA, useful as diagnostic agent for bone
PT disease such as gnathodiaphseal dysplasia, bone deficiency or bone-
PT resorption property disease.
XX
PS Claim 9; SEQ ID NO 2; 11pp; Japanese.
XX
CC The present invention relates to a human gnathodiaphyseal dysplasia (GDD)
CC coding sequence (GDD1; AEH82070) and encoded protein (AEH82071). GDD1 is
CC useful as a bone disease diagnostic agent, where the bone disease is GDD,
CC bone deficiency and/or bone-resorption property disease, where the GDD
CC disease causes hardening of bone, susceptibility to fracture, cement bone
CC pathology of a lower jaw bone, etc. GDD1 is also useful in bone formation
CC regeneration, hard tissue reconstruction, etc., and in research
CC application.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 913 AA;

Query Match 29.4%; Score 1455; DB 11; Length 913;
Best Local Similarity 38.6%; Pred. No. 8.4e-140;
Matches 325; Conservative 154; Mismatches 276; Indels 86; Gaps 22;

Qy 108 RIADFVLVWEEDLKLDRQQDSAARDRTDMHRTWRETFLDNLRAAGL---CVDQQDVQDGN 164
| |||| : :||| | : : | : | || | | : : | : |
Db 78 RQIDFVLSYVDDVKKD-----AELKAERRKEFETNLRKTGLELEIEDKRDSER 127

Qy 165 TTVHYALLSASWAVLCYYAEDLRLKLPLQE--LPNQASNWSAGLLAWLGIPNVLLEVPD 222
| : : | | | | | | : : | : : | : : | : : |
Db 128 T--YFVKIHAPWEVLVTYAEVLGIKMPIKESDIPRPKHTPISYVLGPVRLP--LSVKYPH 183

Qy 223 VPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEK-KNLLGIHQ 281
||| : : | : : | | | | : : | : : | : : | : : | : : |
Db 184 --PEYFTAQFSRHRQELFLIED-QATFFPSSSRNRIVYYILSRCPFIEDGKKRFGIERL 240

Qy 282 LAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQVLFQHWARWGKWNKYQPLDHVRRYFGE 341
| : : | | | | : | | | : | | : : | : : | : : |

Db	241	LNSNTYSSAYPLHDGQYWKPSEPPNP--TNERYTLHQNWARFSYFYKEQPLDLIKNYYGE	298
Qy	342	KVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSK--DSFEMCPLCLD	399
Db	299	KIGIYFVFLGFYTEMLFFAAVVGACFIYGLLSMEHNTSSTEICDPEIGGQMIMCPLCDQ	358
Qy	400	-CPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYE	458
Db	359	VCDYWRLNSTCLASKFSHLFDNESTVFFAIFMGIWVTLFLEFWKQRQARLEYEWDLVDFE	418
Qy	459	DTEE--RPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV	516
Db	419	EEQQQLQLRPEFEAMCKHRKLNNAVTKEMEPYMPPLYTRIPWYFLSGATVTLWMSLVVTSMV	478
Qy	517	SIILYRAIMAIVVSRSGNTLLAAWASRI-----ASLTGSVVNLVFI	558
Db	479	AVIVYRL-----SVFATFASFMESDASLKQVKSFLTPQITTSLTGSCNLFIVIL	527
Qy	559	ILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNIFYSSPVYIAFFKGRFVGYPG	618
Db	528	ILNFFYEKISAWITKMEIPRTYQEYESSLTKMFLFQFVNIFYSSCFYVAFFKGKFGVGYPG	587
Qy	619	NYHTLFGV-RNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLPKLGWWQKFLRLRSK	677
Db	588	KYTYLFNEWRSEECDPGGCLIELTTQLTIIMTGKQIFGNIKEAIIPLALNWW-----R	640
Qy	678	KRKAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTIFVAACPLAPL FALLN	735
Db	641	RRKARTNSEKLYSRWEQDHDLESFGPLGLFYEYLETVTQFGFVTLFVASFPLAPLLALIN	700
Qy	736	NWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAY	795
Db	701	NIVEIRVDAWKLTQYRRTVASKAHSIGVWQDILYGMAVLSVATNAFIVAFTSDIIPRLV	760
Qy	796	YRW---TRAHDLRGFLN----FTLARAPSSFAAAHNR--TCRYRAFR---DDDGHY-	839
Db	761	YYYAYSTNATQPMGTGYVNNLSVFLIADFPNHTAPSEKRDFITCRYRDYRYPPDDENKYF	820
Qy	840	-SQTYWNL LAIRLAFVIVFEHVVF SVGRLLDLLVPDIPESVEIKVKREYYLAKQALAENE	898
Db	821	HNMQFVHVLAAKMTFIIVMEHVFLVKFLLAWMIPDVPKDVVERIKREKLMTIKILHDFE	880
Qy	899	V	899
Db	881	L	881

ID ABB62812 standard; protein; 1219 AA.
XX
AC ABB62812;
XX
DT 15-JUN-2007 (revised)
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 15228.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; BOND_PC; CG6938-PA; CG6938-PA [Drosophila melanogaster];
KW CG6938.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL06915.
DR PC:NCBI; gi24663059.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 15228; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
CC

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.

XX

SQ Sequence 1219 AA;

Query Match 29.2%; Score 1445; DB 4; Length 1219;
Best Local Similarity 35.6%; Pred. No. 1.4e-138;
Matches 342; Conservative 165; Mismatches 332; Indels 122; Gaps 27;

Qy	35	AERWAMTSETSSGSHCARSRML-----RRRAQEEDSTVLIDVSPPEAEKRGSY	82
		: : : : :	
Db	249	ADRVNQSYEVMESH---SNVLPDQFGYRQLIPTERKASDTASSV-----SGSY	294
Qy	83	GSTAHASEP---GGQQAACRAGSPAKP-----RIADFVLVW-EEDLKLDRQ	125
		: : : :	
Db	295	YGSRKASKSNSLGGESGDERRVSKQDREGLDPESLMFRDGRKVDMLAWEEEDLGVMTE	354
Qy	126	QDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQD-VQDGNTTVHYALLSASWAVLCYYAE	184
		:: : : : : :	
Db	355	AEAKRRDN-----RRSFMENLIKEGLEVELEDKSQSFNEKTFFLKIHLPWRLLETRLAE	407
Qy	185	DLRLKLP-----LQELPNQASNWSAGLLAWLGIPNVLLLEVVPDVP	225
		: : : : :	
Db	408	VMNLKLPVKRFITISVKPSWDEENVVLRNMQYWQDVWQR-LTKKIQLDQTLLE---GET	462
Qy	226	EYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEG	285
		: : : : : : : : : : : : : : : :	
Db	463	TFKAATANGNPEEQFIVKD-RATAFTSAQRSLMVMQVLI RTPFDES DRS--GIRRLMNDG	519
Qy	286	VLSAAFPLHDGPFKTPPEGPQAPRLN-QRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVA	344
		: : : : : : : : : : : :	
Db	520	TYLGCFLPLHEGRY----DRPHSSGISLDRRVLYQTWAHPSQWYKKQPLCLVRKYFGDKIA	575
Qy	345	LYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFS--IPTQELCG--SKDSFEMCPLC-LD	399
		: : : : : : :	
Db	576	LYFCWLGFYTEMLVYPVAVGTLCFIYGLATLESEDNTPSKEICNEYGTGNITLCPLCDKA	635
Qy	400	CPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYED	459
		: : : : : : : : : :	
Db	636	CSYQRLSESCFLSRLTYLFDNPSTVFFAIFMSFWATTFLLELWKRKQSVLVWEWDLHNV-D	694
Qy	460	TEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSII	519
		: : : : : : : : : : : : :	
Db	695	MDEENRPEFETNATTFRMNPVTREKEPYMSTWNRSIRFVITGSAVLFMISVVL SAVLGTI	754
Qy	520	LYRAIMAIVVSRSNTLLAAWASRIASLTGSVVNLVFIILISKIYVSLAHVLTRWEMHRT	579
		: : : : : : : :	
Db	755	LYRITLVSVIYGGGGFFVKEHAKLFTSVTAALINLVVIMILTRIYHRMAIKLTNLENPRT	814

